```
   1 TCATTCCAAA CAAGTCAGGA AAGCCTGCAC AGGACTGGAT AAATAATTAA
  51 GAACAGAGTG TTCTGAACAT CAACACAAAG TGGAAGAACC TTAAGCTGAA
 101 GGTACAGTAT ATTATTTACA CTGAAGGGCC TTGTGTGTGG ACAAGAAAGC
 151 GCTGACAGCT CAAATGGATC CCATGGAACT GAGAAATGTC AACATCGAAC
 201 CAGATGATGA GAGCAGCAGT GGAGAAAAAG CTCCAGATAG CTACATCAGG
 251 ATAGGAAATT CAGAAAAGGC AGCAATGTCC AGTCAATTTG CTAATGAAGA
 301 CACTGAAAGT CAGAAATTCC TGACAAAICG ATTTTTGGGG AAAAAGAAGC
 351 TGGCAGATTA TGCTGATGAA CAGCATCCCG GAACCACTTC CTTTGGAATG
 401 TCTTCATTTA ACCTGAGTAA TGCCATCAAG GGCAGTGGGA TCCTGGGCTT
 451 GTCCTATGGC ATGGCCTACA CAGGGTCAT ACTTTTTATA ATCATGCTGC
 501 TTGCTGTGGC AATATTATCA CTGTATTCAG TTCACCTTTT ATTAAAAACA
 551 GCCAAGGAAG GAGGGTCTTT GATTTATGAA AAATTAGGAG AAAAGGCATT
 601 TGGATGGCCG GGAAAAATTG GAGCTTTTCT TTCCATTACA ATGCAGAACA
 651 TTGGAGCAAT GTCAAGCTAC CTCTTTATCA TTAAATATGA ACTACCTGAA
 701 GTAATCAGAG CATTCATGGG ACTTGAAGAA AATACTGGAG AATGGTACCT
 751 CAATGGCAAC TACCTCATCA TATTTGTGTT TGTTGGAATT ATTCTTCCAC
 801 TTTCGCTCCT TAAAAATTTA GGTTATCTTG GCTATACCAG TGGATTTTCT
 851 CTTACCTGCA TGGTGTTTTT TGTTAGTGTG GTGATTTACA AGAAATTCCA
 901 AATACCCTGC CCTCTACCTG TTTTGGATCA CAGTGTTGGA AATCTGTCAT
 951 TCAACAACAC GCTTCCAATG CATGTGGTAA TGTTACCCAA CAACTCTGAG
1001 AGTTCTGATG TGAACTTCAT GATGGATTAC ACCCACCGCA ATCCTGCAGG
1051 GCTGGATGAG AACCAGGCCA AGGGCTCTCT TCATGACAGT GGAGTAGAAT
1101 ATGAAGCTCA TAGTGATGAC AAGTGTGAAC CTAAATACTT TGTATTCAAC
1151 TCCCGGACGG CCTATGCAAT TCCTATCCTA GTATTTGCTT TTGTATGCCA
1201 CCCTGAGGTC CTTCCCATCT ACAGTGAACT TAAAGATCGG TCCCGGAGAA
1251 AAATGCAAAC GGTGTCAAAT ATTTCCATCA CGGGGATGCT TGTCATGTAC
1301 CTGCTTGCCG CCCTCTTTGG TTACCTAACC TTCTATGGAG AAGTTGAAGA
1351 TGAATTACTT CATGCCTACA GCAAAGTGTA TACATTAGAC ATCCCTCTTC
1401 TCATGGTTCC CCTGCCACTC CTTGTGGCAA TAACACAAAC TGTGCCCATT
1451 GTCCTCTTCC CAATTCGTAC ATCAGTGATC ACACTGTTAT TTCCCAAACG
1501 ACCCTTCAGC TGGATACGAC ATTTCCTGAT TGCAGCTGTG CTTATTGCAC
1551 TTAATAATGT TCTGGTCATC CTTGTGCCAA CTATAAAATA CATCTTCGGA
1601 TTCATAGGGG CTTCTTCTGC CACTATGCTG ATTTTTATTC TTCCAGCAGT
1651 TTTTTATCTT AAACTTGTCA AGAAAGAAAC TTTTAGGTCA CCCCAAAAGG
1701 TCGGGGCTTT AATTTTCCTT GTGGTTGGAA TATTCTTCAT GATTGGAAGC
1751 ATGGCACTCA TTATAATTGA CTGGATTTAT GATCCTCCAA ATTCCAAGCA
1801 TCACTAACAC AAGGAAAAAT AC
```

FEATURES:

5'UTR:	1-163
Start Codon:	164
Stop Codon:	1805
3'UTR:	1808

FIGURE 1, page 1 of 2

HOMOLOGOUS PROTEINS:

Top BLAST Hits:

	Score	E
CFA|14500003337444 /altid=gi|12017941 /def=gb|AAG45335.1|AF295...	975	0.0
CFA|14000033649823 /altid=gi|10945621 /def=gb|AAG24618.1|AF298...	597	e-169
CFA|15000003782430 /altid=gi|8577401 /def=gb|AAF75589.2|AF1736...	591	e-168
CFA|14300000720069 /altid=gi|8248427 /def=gb|AAF74195.1|AF2496...	587	e-166
CFA|87000000006802 /altid=gi|7243145 /def=dbj|BAA92620.1| (AB03...	573	e-164
CFA|13000005969115 /altid=gi|5870433 /def=ref|NP_006832.1| tran...	500	e-140
CFA|88000001154721 /altid=gi|7406150 /def=gb|AAF61849.1|AF15985...	496	e-139
CFA|65000019404613 /altid=gi|9506837 /def=ref|NP_061849.1| amin...	495	e-139
CFA|10000000004435450 /altid=gi|8926332 /def=gb|AAF81797.1|AF2730...	492	e-138
CFA|33500010936896 35 /altid=gi|11434147 /def=ref|XP_006635.1| hy...	480	e-134

EST:

gi|10934204 /dataset=dbest /taxon=96...	1078	0.0
gi|10286121 /dataset=dbest /taxon=96...	718	0.0
gi|9872634 /dataset=dbest /taxon=960...	680	0.0
gi|2656674 /dataset=dbest /taxon=9606 ...	549	e-154
gi|9882497 /dataset=dbest /taxon=960...	541	e-151
gi|689641 /dataset=dbest /taxon=9606 /...	525	e-147

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|10934204 Whole embryo (mainly head)
gi|10286121 Hepatocellular carcinoma
gi|9872634 Non-cancerous liver
gi|2656674 Fetal liver spleen
gi|9882497 Non cancerous liver
gi|689641 Liver

Expression information from PCR-based tissue screening panels:

Mixed tissue (Brain, Heart, Kidney, Lung, Spleen, Testis, Leukocyte)

FIGURE 1, page 2 of 2

```
   1 MDPMELPNVN IEPDDESSSG ESAPDSYIRI GNSEKAAMSS QFANEDTESQ
  51 KFLTNGFLGK KKLADYADEH HPGTTSFGMS SFNLSNAIMG SGILGLSYAM
 101 AYTGVILFII MLLAVAILSL YSVHLLLKTA KEGGSLIYEK LGEKAFGWPG
 151 KIGAFVSITM QNIGAMSSYL FIIKYELPEV IRAFMGLEEN TGEWYLNGNY
 201 LGIFVSVGLI LPLSLLKNLG YLGYTSGFSL TCMVFFVSVV IYKKFQIPCP
 251 LPVLPSVGNL LSFNNTLPMH VVMLPNNSES SDVNFMMDYT HRNPAGLDEN
 301 QAKGSLRDSG VEYEAHSDDK CEPKYFVFNS FTAYAIPILV FAFVCHPEVL
 351 KIYSFCKDRS KKMQTVSNI SITCMLVMYL IAALPGYLTF YGEVEDELLH
 401 AYSFVYTLDI PLLMVRLAVL VAVTQTVPIV LFPIKTSVIT LLFPKRPFSW
 451 IRHFLIAAVL IALNNVLVIL VPTIKYIFGF IGASSATMLI FILPAVFYLK
 501 LVKKEIKRSP QFVGALIFLV VGIFFMIGSM ALIIIDWIYD PPNSKHH
```

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 5

1	83-86	NLSN
2	260-263	NLSF
3	264-267	NNTL
4	276-279	NNSE
5	369-372	NISI

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

1	503-506	KRET

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 7

1	33-35	SEK
2	49-51	SQK
3	129-131	TAK
4	290-292	THR
5	360-362	SRR
6	473-475	TIK
7	506-508	TFR

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 5

1	18-21	SSGE
2	22-25	SAPD
3	129-132	TAKE
4	305-308	SLHD
5	309-312	SGVE

[5] PDOC00008 PS00008 MYPISTYL
N-myristoylation site

Number of matches: 6

1	96-100 GLSYAM
2	153-158 GAFVSI
3	164-169 GAMSSY
4	186-191 GLEENT
5	296-301 GLDENQ
6	482-487 GASSAT

[6] PDOC00009 PS00009 AMIDATION
Amidation site

58-61 LGKK

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	79	99	1.125	Certain
2	102	122	2.503	Certain
3	153	173	1.197	Certain
4	197	217	1.785	Certain
5	222	242	2.123	Certain
6	332	352	1.240	Certain
7	370	390	2.166	Certain
8	414	434	1.301	Certain
9	453	473	1.520	Certain
10	476	496	2.166	Certain
11	515	535	2.628	Certain

BLAST Alignment to Top Hit:

>CRA|145000039337444 /altid=gi|12017311
/def=gb|AAG45335.1|AF295535_1 (AF295535) amino acid
transport system A3 [Rattus norvegicus] /org=Rattus
norvegicus /taxon=10116 /dataset=nraa /length=547
Length = 547

Score = 975 bits (2492), Expect = 0.0
Identities = 473/547 (87%), Positives = 508/547 (92%)

```
Query: 1   MDPMELRNVNIEPDDESSGESAPDSYIRIGNSEKAAMSSQFANEDTESQKFLTNGFLGK 60
           MDP+ELR+VNIEP ++S S +S    Y  +GNSEK AM SQFANED ESQKFLTNGFLGK
Sbjct: 1   MDPIELRSVNIEPYEDSCSVDSIQSCYTGMGNSEKGAMDSQFANEDAESQKFLTNGFLGK 60

Query: 61  KELADYADEHHPGTTSFGMSFNLSNAIMGSGILGLSYAMAYTGVILFIIMLLAVAILSL 120
           K L DYADEHHPGTTSFGMSFNLSNAIMGSGILGLSYAMA TG++LF+IMLL VAILSL
Sbjct: 61  KTLTDYADEHHPGTTSFGMSFNLSNAIMGSGILGLSYAMANTGIVLFVIMLLTVAILSL 120

Query: 121 YSVHLLLKTAKEGGSLIYEKLGEKAFGWPGKIGAFVSITMQNIGAMSVYLFIIKYELPEV 180
           YSVHLLLKTAKEGGSLIYEKLGEKAFGWPGKIGAF+SITMQNIGAMSVYLFIIKYELPEV
Sbjct: 121 YSVHLLLKTAKEGGSLIYEKLGEKAFGWPGKIGAFISITMQNIGAMSVYLFIIKYELPEV 180

Query: 181 IEAFMGLEENTGEWYLNGNYLIIFVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSVV 240
           IE FMGLEENTGEWYLNGNYL++FVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSVV
Sbjct: 181 IEVFMGLEENTGEWYLNGNYLVLFVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSVV 240

Query: 241 IYKKFQIPCPLPVLDHSVGNLSFNNTLPMHVVMLPNNSESSDVNFMMDYTHFNPAGLDEN 300
           IYKKFQIPCPLPVLDH+ GNL+FNNTLPMHV+MLPNNSES+ +NFM+DYTHF+P GLDE
Sbjct: 241 IYKKFQIPCPLPVLDHNIGNLTFNNTLPMHVIMLPNNSESTGMNFMVDYTHFDPEGLDEK 300

Query: 301 QAKGSLHDSGVEYEAHSDDKCEPKYFVFNSRTAYAIPILVFAFVCHPEVLPIYSELKDRS 360
            A G LH SGVEYEAHS DKC+PKYFVFNSRTAYAIPIL FAFVCHPEVLPIYSELKDRS
Sbjct: 301 PAAGPLHGSGVEYEAHSGDKCQPKYFVFNSRTAYAIPILAFAFVCHPEVLPIYSELKDRS 360

Query: 361 RRKMQTVSNISITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLDIPLLMVRLAVL 420
           RRKMQTVSNISITGMLVMYLLAALFGYL+FYGEVEDELLHAYSKVYT D  LLMVRLAVL
Sbjct: 361 RRKMQTVSNISITGMLVMYLLAALFGYLSFYGEVEDELLHAYSFVYTFDTALLMVRLAVL 420

Query: 421 VAVTQTVPIVLFPIPTSVITLLFPKRPFSWIRHFLIAAVLIALNNVLVILVPTIKYIFGF 480
           VAVT TVPIVLFPIPTSVITLLFP+RPFSW++HF IAA++IALNNVLVILVPTIKYIFGF
Sbjct: 421 VAVTLTVPIVLFPIPTSVITLLFPRRPFSWVKHFGIAAIIIALNNVLVILVPTIKYIFGF 480

Query: 481 IGASSATMLIFILPAVFYLFLVKKETFRSPQKVGALIFLVVGIFFMIGSMALIIIDWIYD 540
           IGASSATMLIFILPA FYLFLVKKE  RSPQK+GAL+FLV GI FM+GSMALIIIDWIY+
Sbjct: 481 IGASSATMLIFILPAAFYLFLVKKEPLRSPQKIGALVFLVTGIIFMMGSMALIIIDWIYN 540

Query: 541 PPNSKHH 547
           PPN  HH
Sbjct: 541 PPNPDHH 547


>CRA|114000033649823 /altid=gi|10945621
/def=gb|AAG24618.1|AF298897_1 (AF298897) amino acid
transporter system A [Homo sapiens] /org=Homo sapiens
/taxon=9606 /dataset=nraa /length=506
Length = 506

Score = 597 bits (1522), Expect = e-169
Identities = 315/549 (57%), Positives = 383/549 (69%), Gaps = 46/549 (8%)

Query: 1   MDPMELRNVNIEPDDESSSGESAPD---SYIRIGNSEKAAMSSQFANEDTESQKFLTNGF 57
           M   E+   +I PD++SSS  S  D   SY     +++AA+ S +A+ D E+Q FL
Sbjct: 1   MKKAEMGRFSISPDEDSSSYSSNSDFNYSY----PTKQAALKSHYADVDPENQNFLLESN 56
```

Confidential

FIGURE 2, page 3 of 4

```
Query: 58  LGKKFLADYADEHHPGTTSFGMGSFNLSNAIMGSGILGLSYAMAYTGVILFIIMLLAVAI 117
           LGKKF   Y  E HPGTTSFGMG FNLSNAI+GSGILGLSYAMA TG+ LFII+L  V+I
Sbjct: 57  LGKKFFGGYETEFHPGTTSFGMGVFNLSNAIVGSGILGLSYAMANTGIALFIILLTFVSI 113

Query: 118 LSLYSVHLLLKTAKEGGSLIYEKLGEKAFGWPGFIGAFVSITMQNIGAMSSYLFIIKYEL 177
            SLYSVHLLLKTA EGGSL+YE+LG KAFG  GF+ A  SITMQNIGAMSSYLFI+KYEL
Sbjct: 114 FSLYSVHLLLKTANEGGSLVYERLGYKAFGLVGFLAASGSITMQNIGAMSSYLFIVKYEL 173

Query: 178 PEVIPAFMGLEENTGEWYLNGNYLIIFVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFV 237
           P VI+A   +E+ TG WYLNGNYL++ VS+ +ILPLSL +NLGYLGYTSG SL CMVFF+
Sbjct: 174 PLVIQALTNIEDKTGLWYLNGNYLVLLVSLVVILPLSLFRNLGYLGYTSGLSLLCMVFFL 233

Query: 238 SVVIYKKFQIPCPLPVLDHSVGNLSFNNTLPMHVVMLPNNSESSDVNFMMDYTHRNPAGL 297
            VVI KKFQ+PCP+       + N + N TL      ++P
Sbjct: 234 IVVICKKFQVPCPVEAA--LLNETINTTLTQPTALVP---------------------- 269

Query: 298 DENQAFGSLHDSGVEYEAHSDFCEPKYFVFNSRTAYAIPILVFAFVCHPEVLPIYSELK 357
                      + +    +D C P YF+FNS+T YA+PIL+F+FVCHP VLPIY ELK
Sbjct: 270 ------------ALSHNVTENDCRPHYFIFNSQTVYAVPILIFSFVCHPAVLPIYEELK 317

Query: 358 DRSRFKMQTVSNISITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLDIPLLMVRL 417
           DRSRF+M  VS IS   M +MYLLAALFGYLTFY  VE ELLH YS +   DI LL+VRL
Sbjct: 318 DRSRFFMMNVSKISFFAMFLMYLLAALFGYLTFYEHVESELLHTYSSILGTDILLLIVRL 377

Query: 418 AVLVAVTQTVPIVLFPIPTSVITLLFPKPPFSWIRHFLIAAVLIALNNVLVILVPTIKYI 477
           AVL+AVT TVP+V+FPIP+SV  LL   + FSW RH LI   ++A  N+LVI VPTI+ I
Sbjct: 378 AVLMAVTLTVPVVIFPIPSSVTHLLCASKDFSWWRHSLITVSILAFTNLLVIFVPTIRDI 437

Query: 478 FGFIGASSATMLIFILPAVFYLKLVKKETFRSPQKVGALIFLVVGIFFMIGSMALIIIDW 537
           FGFIGAS+A+MLIFILP+ FY+KLVKKE  +S QK+GAL FL+ G+  M GSMALI++DW
Sbjct: 438 FGFIGASAASMLIFILPSAFYIKLVKKEPMKSVQKIGALFFLLSGVLVMTGSMALIVLDW 497

Query: 538 IYDPPNSKH 546
           +++ P   H
Sbjct: 498 VHNAPGGGH 506
```

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF01490	Transmembrane amino acid transporter protein	187.0	2.9e-52	2
CE00398	E00398 CD53	4.0	4.8	1

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
CE00398	1/1	90	110	..	1	23	[.	4.0	4.8
PF01490	1/2	99	236	..	1	179	[.	58.9	2.5e-14
PF01490	2/2	305	529	..	200	467	.]	133.9	3e-36

FIGURE 2, page 4 of 4

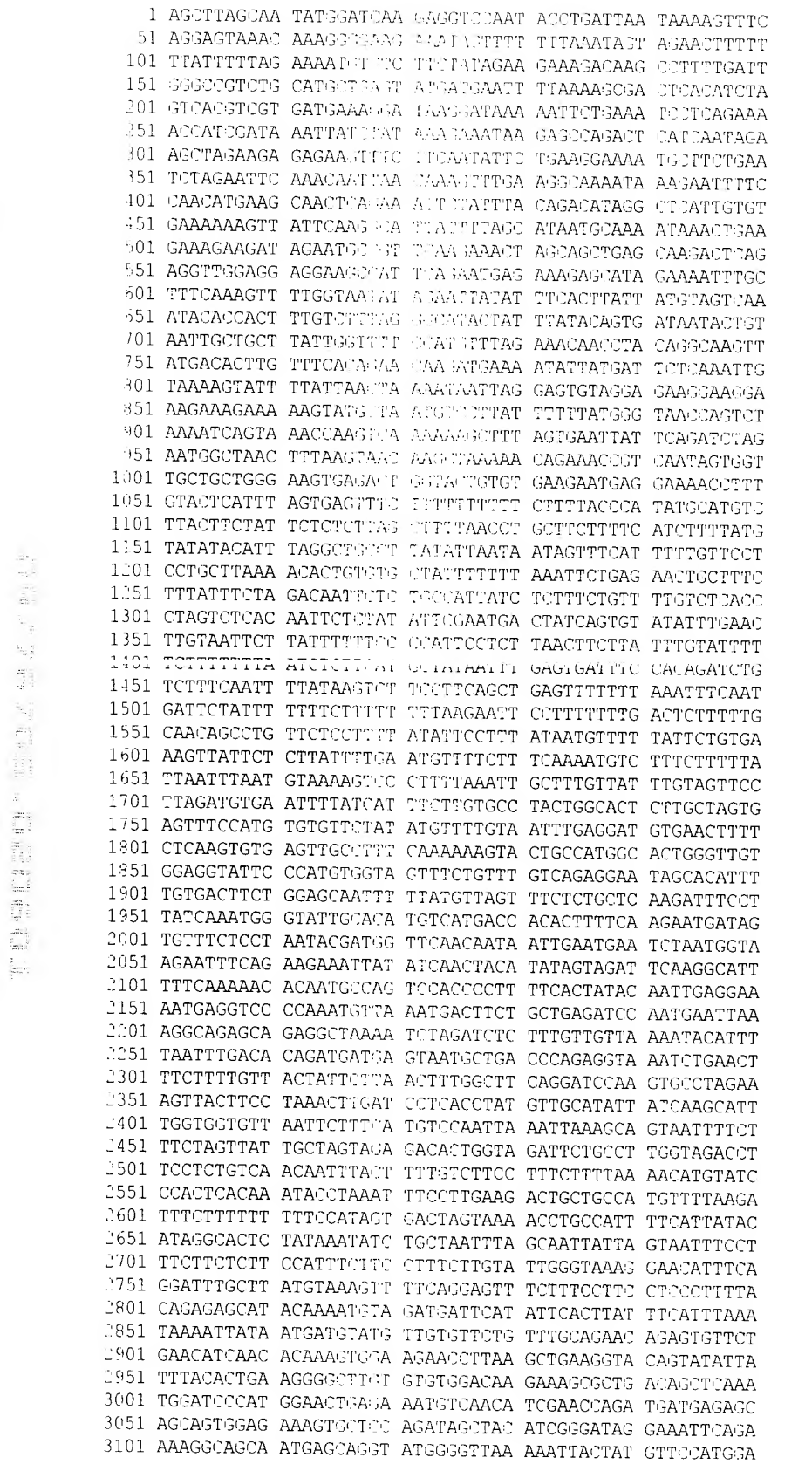
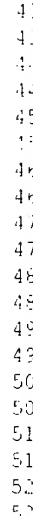


FIGURE 3, page 1 of 23



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3151 AAAATAAGAC AGGATGTGGA CATGGAAAAC AGGGTCTTGA TGGGAAGAAC
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3251 ATCAATTCCC TGGTCCTGAA ATACAGTGAT AATGTCAATC TCTTTTGTGA
3301 CTGATCTAGA ATTGAGGTTA CAATGTCTTT GTCTCCATTA ATAATGTGTA
3351 ATAATTTTAA TTATTTTATC CTATTGCTCC TCTTATCTTT CTCAGATTCC
3401 TCTTTGAATG TTGCTACACC TCCTGGTTTC TGTAGGGATT CTTTTCTCTC
3451 TAAAAGTATC CTCTGGGCAA GCTCACTCAC AACTACTATG GCCTCACCCT
3501 CCAAATATAT GCCATATACC CAGCCTGTTA AGTTTCTCTA CTGAATTTCA
3551 GATAATTATA TCTGAATGTC TACTGCACGT CTCTACTGGA CCATTACTGT
3601 GTCTAAATTG CCTCATTTAT AAAGTTAAAC CTGTAATGTC TAATACTGAA
3651 CTCCTATCTT TCCCTCCAAA ACCCTGCTCC CCTCTACTAA TCCCCATCCT
3701 AGTGAAAATC ACTGCTATCA TGTAGCAACT CACTCAAAAG CCCCTAGGTG
3751 TAAACTTTGA CCCACATAGC CAACGGTCAG TCATATCCAG TTAGTTGAAC
3801 CTTATTAATG CTTCAAATAC ACCTACTTTT CTGTACCCAT TCTACTGTGG
3851 TCTTACGTTA GGCCTACATT AAATGTGAGA CAGGGAGAGA GCCCTGATCT
3901 CTCTCCCTGT CTTACATTTT GCCTTCCTCT GTCTAGCCCT CTACATTCCT
3951 GCAAGAGCAA TCTCTTACAA TTGCAAATTG AATCAATTTC CATCCTTAGA
4001 TAAAGCCCTT CTGCACCTCT CCAATAGCCA TAACAGAAAG TAGATTACAC
4051 ACACTGCTGG GCAGGTAAGG TCCTTGTGGA TCTGTTCTTG ACCTGGCCCT
4101 CCTGTCCTGT TTTTTGCCCT CTCCCTATTT GTTACTTGTT GCCTTCACTC
4151 ATTCTGCTCC AACTGCCTGG AATCAGTCAC CTGCTCCCCC TTCTCCCGTG
4201 TTGACACCTC TCATCCTTCA AGAATCAGCT CAACATCAGG TCTCCTATGC
4251 AGCCTTTTCC AAATTACTCT ACTCCCCCAT GTAGAAGTGA CTGGCCCTCC
4301 TTCATGTACC CTCTCCCTGT GCAGATGTTA ATTACGCCAC TACTACAGGT
4351 TAATGGCCTC TGTGGTCCCA CCACCTGCCA CATTGTCTGG TGCATAGTGA
4401 GTGCACAATA GTTATTTGAT AAGTCAATTG ATTTCCCACA AAATGTTATA
4451 TCAAATTGTA CATGATTTAA GATGCTCAGA AGGGAATTTT TCACCAAATC
4501 TAGGCGTGAA ATAGAGAATA TTGTGCTCAA ACAAAGACTT CTCATTTTAT
4551 TTACAACACC CAGGAAAATC CACCAGGAGA AACTACCGTT CTTCCTTCAA
4601 GTAGCTCAGT GCAATGAACT TTAGGGATGT CGGACTAGAG AGGCCACTGA
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4801 AACCAACAGC TGCTTTTCAA GGATGAGATG GGTGACCAGA ATATAGATGA
4851 CATTCAATAC TTTTTTATTA CTTCTCCTTC ACTGCATTAC CCTCAGTAAA
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4951 TCTGCCGAGG TTGACAGAGT TAAAGGGGAC ACCCTCCTAA GAACTGTCAT
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5051 CTTTTCTTAA GCTTCATGCA ATGTGTTCCG AACCACTCAC AGTGACTTAC
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5201 AATGTAAATT TTTGAGAAAT TCAACATAAT GTATTTATTT GTGATCATTA
5251 TACTTGTGTT TTCAATACAT GCTGGGTTTG GTATCAAAAC ATTTAACATA
5301 CTGGGGACAT TTCTCATCTA TTTTATACAA TCTTGGCATG TTAAATGACT
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5451 GATTTTAGTT TATTGATTAA AATAAAGATT CCAGAGTTTA AATTCTAGGT
5501 GGCACTTTTG TTTTTATAGT CCTCAGGCCC ATTTTAGGCT TCATTTTATC
5551 CTGTCATCTC AGTCTCCAAC TGTGAACATT ATGTACCAGT CTTCACATAG
5601 CAGGTACATT AATTACAGAC CATTAATGTA AACCACAAAA GAGTGGTGGG
5651 CAGTGGGTGG GGGGTGAATG GAAATGGAAA GAGGCAACAA CTGAGGGCAT
5701 TGTGCTTTCT GTGAGAAATA TGGGGAGAAG GCTAGGAAAT GTTCTTAACT
5751 TGTGTACTCA GAGCTATTTA TGCCTTGAGT TCTAGAAAAG CACATACAAC
5801 TTTGTGGTTT CGTGTGCTGT TTCTATCTAC ATCTCATACT GTTTTCTATT
5851 CTCAAAAAGT AACCCTGTCA TCCTCTTTCC TCTCCAGATT ATTTTCAGGA
5901 TTAGCTTCTG TTATAAAAAA TAGCTTGTAC AGATCTCCTA CAATAATTAT
5951 TTTCTATTTT ATTTCTAAGG TTTATTTATT TATTTATTGA GACAGACAGA
6001 GTTTCACTCT TGTGGCCCAT GCTGGAGTGC AATGGTGCAA TCTCGGCTCA
6051 CTGCAACCTC TGCCTCCCAG GTTCAAGCGA TTCTCCTGCT TCAGCCTCCT
6101 GAGTAGCTGG GATTACAGGC GCCTGCCACC ACACTCGGCT AATTTTTTGT
6151 ATTTCTAGTA GAGACGAAGT TTCACCATGT TGGCCAGGCT GGTCTTGAAC
6201 TCCTGACCTC AAGTTATCCA CCCACCTCAG CCTCCCAAAG TGCTGGGATT
6251 ACAGGCGTGA GCCACTGTGC CTGGCCTCTA GGATTATATT AATAGAACAA
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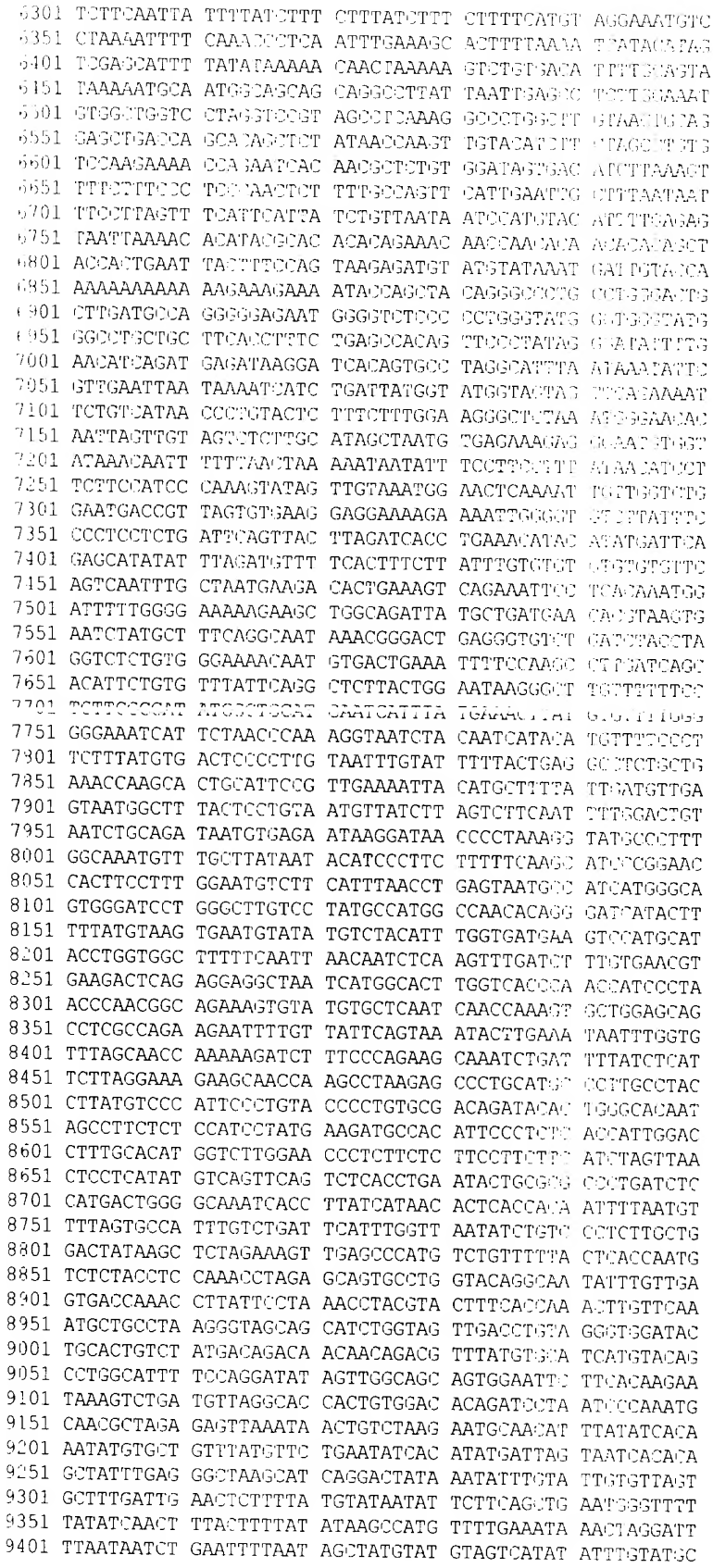
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6351 CTAAAATTTT CAAACCCTCA ATTTGAAAGC ACTTTTAAAA TCATACATAG
6401 TCGAGCATTT TATATAAAAA CAACTAAAAA GTCTGTGACA TTTTCAAGTA
6451 TAAAAATGCA ATGGCAGCAG CAGGCCTTAT TAATTGAGTC TCCTCAAAAT
6501 GTGGCTGGTC CTAGGTCCGT AGCCTCAAAG GCCCTGGCTT GTAACTGCAG
6551 GAGCTGAGCA GCACAGCTCT ATAACCAAGT TGTACATCTT CTAGCTTGTG
6601 TCCAAGAAAA CCAGAATCAC AACGCTCTGT GGATAGTGAC ATCTTAAAGT
6651 TTTGTTTCCC TCCTAACTCT TTTGCCAGTT CATTGAATTG CTTTAATAAT
6701 TTCCTTAGTT TCATTCATTA TCTGTTAATA ATCCATGTAC ATCTTGAGAG
6751 TAATTAAAAC ACATACGCAC ACACAGAAAC AACCAACACA ACACACAGCT
6801 ACCACTGAAT TACTTTCCAG TAAGAGATGT ATGTATAAAT GATTGTACCA
6851 AAAAAAAAAA AAGAAAGAAA ATACCAGCTA CAGGGCCCTG CCTGTGACTG
6901 CTTGATGCCA GGGGGAGAAT GGGGTCTCCC CCTGGGTATG GCTGCCTATG
6951 GGCCTGCTGC TTCAGCTTTC TGAGCCACAG CTCCCTATAG GAATATTTTG
7001 AACATCAGAT GAGATAAGGA TCACAGTGCC TAGGCATTTA ATAAATATTC
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7501 ATTTTTGGGG AAAAAGAAGC TGGCAGATTA TGCTGATGAA CACGTAAGTG
7551 AATCTATGCT TTCAGGCAAT AAACGGGACT GAGGGTGTCT CATCTACCTA
7601 GGTCTCTGTG GGAAAACAAT GTGACTGAAA TTTTCCAAGC CTTGATCAGC
7651 ACATTCTGTG TTTATTCAGG CTCTTACTGG AATAAGGGCT TGTTTTTTCC
7701 TCTTCCCCAT ATGGCTGCAT CAATCATTTA TGAAACTTAT GTGTTTGGG
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7851 AAACCAAGCA CTGCATTCCG TTGAAAATTA CATGCTTTTA TTGATGTTGA
7901 GTAATGGCTT TACTCCTGTA ATGTTATCTT AGTCTTCAAT TTTGGACTGT
7951 AATCTGCAGA TAATGTGAGA ATAAGGATAA CCCCTAAAGG TATGCCCTTT
8001 GGCAAATGTT TGCTTATAAT ACATCCCTTC TTTTTCAAGC ATCTCGGAAC
8051 CACTTCCTTT GGAATGTCTT CATTTAACCT GAGTAATGCC ATCATGGGCA
8101 GTGGGATCCT GGGCTTGTCC TATGCCATGG CCAACACAGG GATCATACTT
8151 TTTATGTAAG TGAATGTATA TGTCTACATT TGGTGATGAA GTCCATGCAT
8201 ACCTGGTGGC TTTTTCAATT AACAATCTCA AGTTTGATCT TTGTGAACGT
8251 GAAGACTCAG AGGAGGCTAA TCATGGCACT TGGTCACCCA ACCATCCCTA
8301 ACCCAACGGC AGAAAGTGTA TGTGCTCAAT CAACCAAAGT GCTGGAGCAG
8351 CCTCGCCAGA AGAATTTTGT TATTCAGTAA ATACTTGAAA TAATTTGGTG
8401 TTTAGCAACC AAAAAGATCT TTCCCAGAAG CAAATCTGAT TTTATCTCAT
8451 TCTTAGGAAA GAAGCAACCA AGCCTAAGAG CCCTGCATGC CCTTGCCTAC
8501 CTTATGTCCC ATTCCCTGTA CCCCTGTGCG ACAGATACAC TGGGCACAAT
8551 AGCCTTCTCT CCATCCTATG AAGATGCCAC ATTCCCTCTC ACCATTGGAC
8601 CTTTGCACAT GGTCTTGGAA CCCTCTTCTC TTCCTTCTTC ATCTAGTTAA
8651 CTCCTCATAT GTCAGTTCAG TCTCACCTGA ATACTGCGCG CCCTGATCTC
8701 CATGACTGGG GCAAATCACC TTATCATAAC ACTCACCACA ATTTTAATGT
8751 TTTAGTGCCA TTTGTCTGAT TCATTTGGTT AATATCTGTC CCTCTTGCTG
8801 GACTATAAGC TCTAGAAAGT TGAGCCCATG TCTGTTTTTA CTCACCAATG
8851 TCTCTACCTC CAAACCTAGA GCAGTGCCTG GTACAGGCAA TATTTGTTGA
8901 GTGACCAAAC CTTATTCCTA AACCTACGTA CTTTCACCAA ACTTGTTCAA
8951 ATGCTGCCTA AGGGTAGCAG CATCTGGTAG TTGACCTGTA GGGTGGATAC
9001 TGCACTGTCT ATGACAGACA ACAACAGACG TTTATGTGCA TCATGTACAG
9051 CCTGGCATTT TCCAGGATAT AGTTGGCAGC AGTGGAATTC TTCACAAGAA
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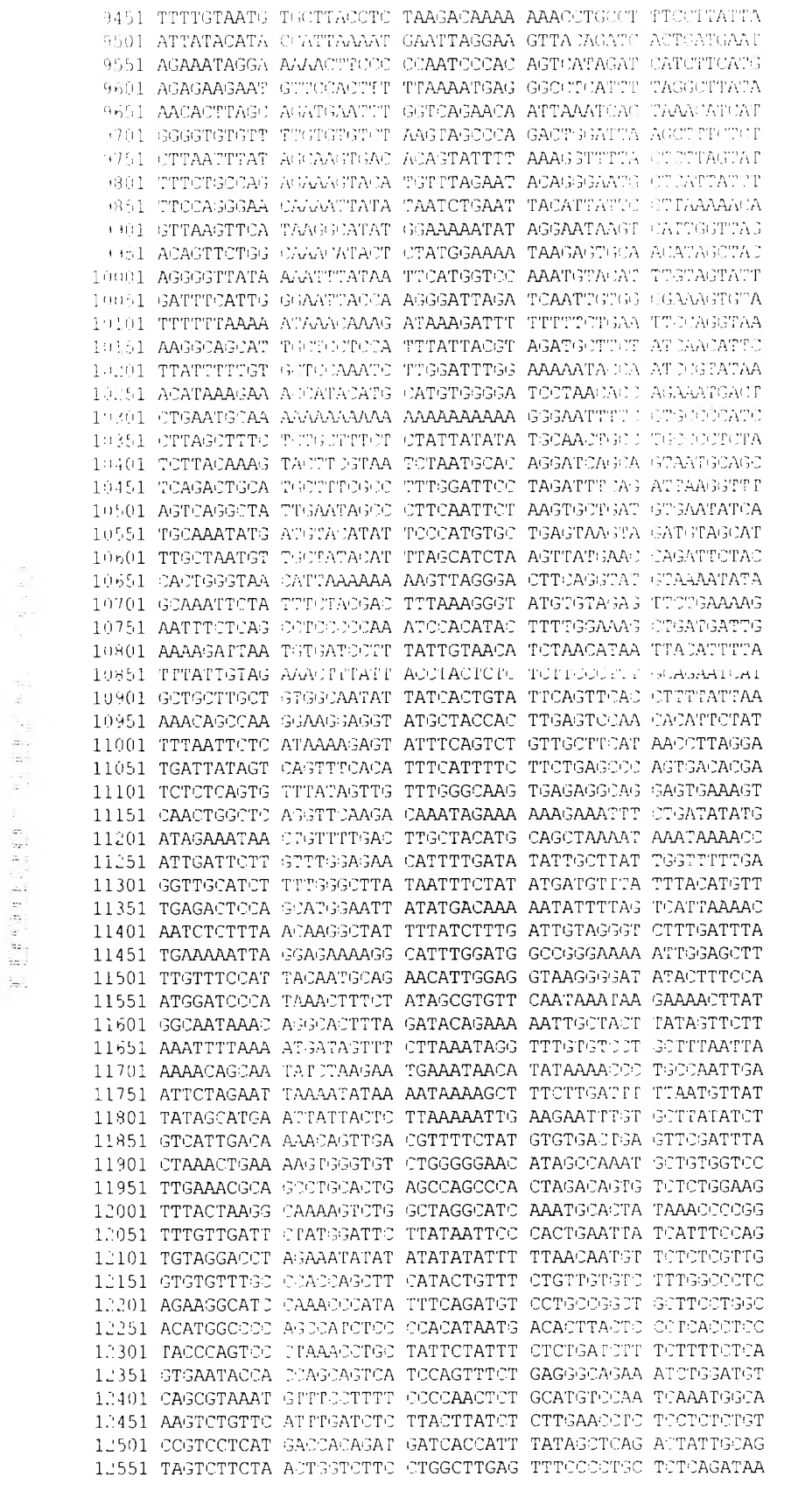

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 9601 AGAGAAGAAT GTTCCACTTT TTAAAATGAG GGCCTCATTT TAGGCTTATA
 9651 AACACTTAGC AGATGAATTT GGTCAGAACA ATTAAATCAG TAAACATCAT
 9701 GGGGTGTGTT TTGTGTGTCT AAGTAGCCCA GACTGGATTA AGCTTTCTCT
 9751 CTTAATTTAT AGCAAGTGAC ACAGTATTTT AAAGTTTTTA CCTTTAGTAT
 9801 TTTCTGCCAG AGAAAGTACA TGTTTAGAAT ACAGGGAATG CTCATTATTT
 9851 TTCCAGGGAA CAAAATTATA TAATCTGAAT TACATTATTC GTTAAAAACA
 9901 GTTAAGTTCA TAAGGCATAT GGAAAAATAT AGGAATAAGT CATTGGTTAG
 9951 ACAGTTCTGG CAAACATACT CTATGGAAAA TAAGAGTGCA ACATAGCTAC
10001 AGGGGTTATA AAATTTATAA TTCATGGTCC AAATGTACAT TGGTAGTATT
10051 GATTTCATTG GGAATTACCA AGGGATTAGA TCAATTGTGG CGAAAGTGTA
10101 TTTTTTAAAA ATAAACAAAG ATAAAGATTT TTTTTCTGAA TTCCAGGTAA
10151 AAGGCAGCAT TGCTGCTCCA TTTATTACGT AGATGCTTCT ATTAACATTC
10201 TTATCTTTGT GTTCCAAATC TTGGATTTGG AAAAATACCA ATCGGTATAA
10251 ACATAAAGAA AACATACATG CATGTGGGGA TCCTAACACC AGAAATGACT
10301 CTGAATGCAA AAAAAAAAAA AAAAAAAAAA GGGAATTTTT GTGCCCATCC
10351 CTTAGCTTTC TCTGCTTTCT CTATTATATA TGCAACTGCC TGCCCCTCTA
10401 TCTTACAAAG TACTTCGTAA TCTAATGCAC AGGATCAGCA GTAATGCAGC
10451 TCAGACTGCA TGCTTTCGCC TTTGGATTCC TAGATTTCAG ATTAAGGTTT
10501 AGTCAGGCTA TTGAATAGCC CTTCAATTCT AAGTGCTGAT GTGAATATCA
10551 TGCAAATATG ATGTACATAT TCCCATGTGC TGAGTAAGTA GATGTAGCAT
10601 TTGCTAATGT TGCTATACAT TTAGCATCTA AGTTATGAAC CAGATTCTAC
10651 CACTGGGTAA CATTAAAAAA AAGTTAGGGA CTTCAGGTAT GTAAAATATA
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10751 AATTTCTCAG CCTCCCCCAA ATCCACATAC TTTTGGAAAG CTGATGATTG
10801 AAAAGATTAA TGTGATCCTT TATTGTAACA TCTAACATAA TTACATTTTA
10851 TTTATTGTAG AAACTTTATT ACCTACTCTC TCTTCCCTTT GCAGAATCAT
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11001 TTTAATTCTC ATAAAAGAGT ATTTCAGTCT GTTGCTTCAT AACCTTAGGA
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11101 TCTCTCAGTG TTTATAGTTG TTTGGGCAAG TGAGAGGCAG GAGTGAAAGT
11151 CAACTGGCTC AGGTTCAAGA CAAATAGAAA AAAGAAATTT CTGATATATG
11201 ATAGAAATAA CTGTTTTGAC TTGCTACATG CAGCTAAAAT AAATAAAACC
11251 ATTGATTCTT GTTTGGAGAA CATTTTGATA TATTGCTTAT TGGTTTTTGA
11301 GGTTGCATCT TTTGGGCTTA TAATTTCTAT ATGATGTTTA TTTACATGTT
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11451 TGAAAAATTA GGAGAAAAGG CATTTGGATG GCCGGGAAAA ATTGGAGCTT
11501 TTGTTTCCAT TACAATGCAG AACATTGGAG GTAAGGGGAT ATACTTTCCA
11551 ATGGATCCCA TAAACTTTCT ATAGCGTGTT CAATAAATAA GAAAACTTAT
11601 GGCAATAAAC AGGCACTTTA GATACAGAAA AATTGCTACT TATAGTTCTT
11651 AAATTTTAAA ATGATAGTTT CTTAAATAGG TTTGTGTCCT GCTTTAATTA
11701 AAAACAGCAA TATCTAAGAA TGAAATAACA TATAAAACCC TGCCAATTGA
11751 ATTCTAGAAT TAAAATATAA AATAAAAGCT TTCTTGATTT TTAATGTTAT
11801 TATAGCATGA ATTATTACTC TTAAAAATTG AAGAATTTGT GCTTATATCT
11851 GTCATTGACA AAACAGTTGA CGTTTTCTAT GTGTGACTGA GTTCGATTTA
11901 CTAAACTGAA AAGTGGGTGT CTGGGGGAAC ATAGCCAAAT GCTGTGGTCC
11951 TTGAAACGCA GCCTGCACTG AGCCAGCCCA CTAGACAGTG TCTCTGGAAG
12001 TTTACTAAGG CAAAAGTCTG GCTAGGCATC AAATGCACTA TAAACCCCGG
12051 TTTGTTGATT CTATGGATTC TTATAATTCC CACTGAATTA TCATTTCCAG
12101 TGTAGGACCT AGAAATATAT ATATATATTT TTAACAATGT TCTCTCGTTG
12151 GTGTGTTTGC CCAGCAGCTT CATACTGTTT CTGTTGTGTC TTTGGCCCTC
12201 AGAAGGCATC CAAAGCCATA TTTCAGATGT CCTGCCGGGT GCTTCCTGGC
12251 ACATGGCCCC AGCCATCTCC CCACATAATG ACACTTACTC CCTCACCTCC
12301 TACCCAGTCC TTAAACCTGC TATTCTATTT CTCTGATCTT TCTTTTCTCA
12351 GTGAATACCA CCAGCAGTCA TCCAGTTTCT GAGGGCAGAA ATCTGGATGT
12401 CAGCGTAAAT GTTTCCTTTT CCCCAACTCT GCATGTCCAA TCAAATGGCA
12451 AAGTCTGTTC ATTTGATCTC TTACTTATCT CTTGAACCTC TCCTCTCTGT
12501 CCGTCCTCAT GACCACAGAT GATCACCATT TATAGCTCAG ACTATTGCAG
12551 TAGTCTTCTA ACTGGTCTTC CTGGCTTGAG TTTCCCCTGC TCTCAGATAA
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FIGURE 3, page 4 of 23

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12701 AAACTTAAAC TCATTGGACT GACACAAGAT CTTCGTCTAG TTCTTCTGCT
12751 CAATCTTTCT AAACTTTCCT AGCAATGCCC ATATCTATCT ATCTTTATCT
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13251 GTGAACTTGG GAAGATCACT GTACTCCTTT GTCTGATTTT TTCATGTATA
13301 AAAATTACCT TACAAAGGCT ATTGTGAGGA TGAAATAAGG TAACATATGG
13351 CACATAATAA GTGTTCTGTA TATGCTTCTC TCCTCCCTGG TTCTCTGCTT
13401 CCATATCCAT GTCTCTGGAG TTGCCTGAAT TATTTTTTAA ATAGGCATTT
13451 AAAAAATTAT AAAACAAATA TATGATGATT GTGAAAAACT AAAACACTGC
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13701 TTTGAGGTTT CCATTACACA AATGTGCCAT AATTTGTTTA CAGTATCCTT
13751 ATTGATGAAC AGTTGGATTG TTTCTAATTT TTCACTGTTA TAAAAATGCT
13801 ACAGTAAATA CACTTGCACA GAGATCTTGC AAACAGGCAA CCCATTTTAA
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15701 AGACTACTGC CCAAGTTATA GACACTAACA CAGGCACACT GAGTATGGGC
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18201 CTAACCCTTG TCTAGAACAC ATTCATTACA AGAGATGTGT CAATATCTGT
18251 CCTTTGTTGT CTTATTTGTA CAATAGAGTC ACTGGCTAGA AAATCTTGTT
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18751 GCTTTCTATG TTAGGAGCCT GTTTCATCTT TATGTTAATT ATATTCTTAT
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18851 GGAAATGATT GTTTTTAAGA CTGAAGGACT AGTGTTTAAG AAAAATGGAA

FIGURE 3, page 6 of 23

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19201 ATATGCAAAT CCTTGTTAGG CTGGTCCTTG ACCTGGGTAG GTATGATTTT
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19301 ATATACTATT TTAGTTTTGT CACTTGACCT GAGGAAATGG GGCCTGATTC
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19701 GACAGAATTT CCTTCAATCT AAGAATGCAC CACCAAAAAA AAGTGACTAT
19751 GGCCACATTA GATTATGCCT GTAACATTTC CTCTCTGGCA TCTTAACAGT
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19951 TAACTTAATT TTTTTCTTAC TGACTTGGTA AATTGAATTG CATGTATGAC
20001 AAATTGTGGA GGAAAAGATT CAGGAGTAGG CCACCATTTG CTTAGGTTTT
20051 TTTTCTATTT GACTAATATT TGACTATTAA CCAAACATGT GCTTTAGATT
20101 GGGCATTAAC TTTTTGCCGG TTGTGAAATA ATGAATGACG AGGTCAATAC
20151 TACTGAAGGT ATTTTCACTA CTTTTTGTCT GATCTTGAGG TGAAAATCCA
20201 ACTACGCTTG ATTCCATAGA TATTTTCTTG TTATTTGTGC TTGGAGTCCT
20251 GAATGAAGGT GTTTTCAAGT AGGGCTGCAT CTTCGTCTTA GAGTAGTACC
20301 CACTGCGAGA CCATCTAAAA ATTATACTAA TTTATCCCTG CACGTTACTT
20351 ATACTTATTT TAATGAGTTT CATAAGACAA GCAAAAACTT GAAAGAGCCC
20401 AAAAATATCT GTTTTAGTGT GGTGATGGAG TCATAGTTGT TGAGCTTGAA
20451 AAAATGGTAG CAATCATTCA TCCTAGAGTT TACACACTGG GTTTGTAACC
20501 TGCATCAGGA GTGGCTGCAC AGGTAGGGAC AGGGGAGGTG GTAGGCTGGG
20551 AGAGACAATA TGTGGGGCTT GGGTCTCTCA TCCCCTTCAA CAAGAGCACC
20601 TTGGTCTCTG TCTGATTTGT AATTGCTTCT GTACAGCGGA GATAGATTTA
20651 TCACAATGTA AATGAGCTTG AGAGGCTCTT TATTTTGTAT TATACCTTCT
20701 GCAACGTTAT CAGCTTCAGG ACCTCTTTGT TCATTTGAAT GAAGGTTGCA
20751 TAGCTAATGA GCTCAGAGGC AAGACCAGAG GTGCCTGGAT TCCCAGGCCT
20801 AGGTCTTTTC CTCTGTTCTG TGTTCTCTCT ATAAAATGTT GCCATAAGTG
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20901 GTAGGAGAAG TTGAAGATGA ATTACTTCAT GCCTACAGCA AAGTGTATAC
20951 ATTAGACATC CCTCTTCTCA TGGTTCGCCT GGCAGTCCTT GTGGCAGTAA
21001 CACTAACTGT GCCCATTGTC CTCTTCCCAG TAAGTACATA AGACTTTGAT
21051 GAAAGAAACC TACTTGACCC CATAAATTAG TACATGTGTT CTACCTTCAT
21101 TTTGATTTAA TTATAGGGTG AGTTTGCAAT TGCAATGCCT GAGGATATTA
21151 TTTTCCTATA GCATTTTGAG TCACTTAAAA TTGGCCATTT AATGTGTAGA
21201 TAGAGCAAGT AGTTTCAGGT GGTATTTTTA TAGTGTAGGA AAAAAATCAT
21251 AAAACTTATT TTTAAACTCA AAGTTGAAAA GTGGAGCTGG AGCTTCTGTC
21301 TTGTGGATTA GTAAAACTGA GTAGGAGTTC ATATAACTTT GGAACCTTGA
21351 AAGCCAAAAC CATATTAACT TTCAAATCTT ATTAAATTTC ATCACAGTTT
21401 TGAAGGCATT TCATTTTTTT TTCAGTTTGT TGTGCTGCAA TAATATACAA
21451 AAGTTGCCTT TTTTAACCTG ATGCCTTGAA GGCTAATGAA AAGGGGATTC
21501 ATGTTAAGTA AATTATATAC CAGAAAAAAA TTTTTCAAAA AACAGTTATG
21551 CTATCTATCA CATATCTCTC TCACACATGG CCTCTGCCAG ACTCACACCA
21601 GGTCACCCCT CCCTGGCATT TGTCATTGGT GTCAGTTTGT TCTGAGATCC
21651 CAGAGCAGAG CTGGTAGTGA AGATTTGGGC TGTGTGAGTT AAAACCAGCA
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21801 AACCAGCACT GTCCTGGACA TAATGTTCCA TACAGGGCTG GCATATGAAG
21851 ACTATTTCTA TAATGACACT GTGGTCACTT TAAATGCAGC TTGTGTGCTG
21901 AAATATATTT TGGCACATTC CTTTTTCATG AGTGCATGAA ATCAGATCCG
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22001 TATATCTGAA AGTATTTCAG ATGACATACA CATAGCTTTA GCCTAAAATC
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25201 TTCCCATCTC TGCACCTTAA GTGACTTCAG AACTAAAATT TTAAAGTGAA
25251 CATCAATCAC AGCATTTCCA AAAATGTGAA CTCCTAGCTT AACCGAAGTA
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FEATURES:

Start:	3000
Exon:	3000-3118
Intron:	3119-7452
Exon:	7453-7543
Intron:	7544-8039
Exon:	8040-8155
Intron:	8156-10894
Exon:	10895-10968
Intron:	10969-11437
Exon:	11438-11530
Intron:	11531-16047
Exon:	16048-16129
Intron:	16130-16215
Exon:	16216-16298
Intron:	16299-16408
Exon:	16409-16467
Intron:	16468-17301
Exon:	17302-17577
Intron:	17578-17709
Exon:	17710-17789
Intron:	17790-19073
Exon:	19074-19174
Intron:	19175-20904
Exon:	20905-21029
Intron:	21030-26649
Exon:	26650-26794
Intron:	26795-27670
Exon:	27671-27768
Intron:	27769-29273
Exon:	29274-29372
Stop:	29373

CHROMOSOME MAP POSITION:

Chromosome 12

ALLELIC VARIANTS (SNPs):

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
1386	T	C	Beyond ORF(5')			
2594	T	C	Beyond ORF(5')			
2757	G	T	Beyond ORF(5')			
6107	C	T	Intron			
6392	T	C	Intron			

9484	C	G	Intron			
10038	A	G	Intron			
10097	G	A	Intron			
10331	G	A	Intron			
10536	T	C	Intron			
11548	T	C	Intron			
11917	G	T	Intron			
12840	T	-	Intron			
12844	A	-	Intron			
12847	T	-	Intron			
13019	C	-	Intron			
13022	A	G	Intron			
13285	G	A	Intron			
14461	G	C	Intron			
15464	-	G	Intron			
15469	-	A	Intron			
15545	T	-	Intron			
16199	T	C	Intron			
16798	T	C	Intron			
18103	C	T	Intron			
18421	A	G	Intron			
18528	G	A	Intron			
18722	T	C	Intron			
18775	C	G	Intron			
18951	T	C	Intron			
18974	T	G	Intron			
19540	A	C	Intron			
19841	G	A	Intron			
20170	A	C	Intron			
20343	T	C	Intron			
20519	G	A	Intron			
20963	T	C	Exon	411	P	P
21840	G	T	Intron			
22783	C	T	Intron			
22787	G	A	Intron			
22825	T	C	Intron			
22967	A	T	Intron			
23248	A	G	Intron			
23764	G	T	Intron			
23765	C	T	Intron			
24432	A	G	Intron			
24538	C	G	Intron			
24693	T	C	Intron			
24819	C	T	Intron			
25743	C	T	Intron			
26044	G	C	Intron			
26555	G	A	Intron			
27886	A	C	Intron			
31884	T	C	Beyond ORF(3')			
32229	T	A	Beyond ORF(3')			

Context:

DNA
Position

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TTAAAACACTGTGTGCTATTTTTTTAAATTCTGAGAACTGCTTTCTTTATTTCTAGACAA
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[T,C]
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2594 CTGAACTTTCTTTTTGTTACTATTCTTAACTTTGGCTTCAGGATCCAAGTGCCTAGAAAGT
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TCTTTCATGTTCAATTAAATTAAAGCAGTAATTTTCTTTCTAGTTATTGCTAGTAGAGAC
ACTGGTAGATTCTGCCTTGGTAGACTTCCTCTGTCAACAATTTACTTTTGTCTTCCTTT
CTTTTAAAACATGTATCCCACTCACAAATACCTAAATTTCCTTGAAGACTGCTGCCATGT
[T,C]
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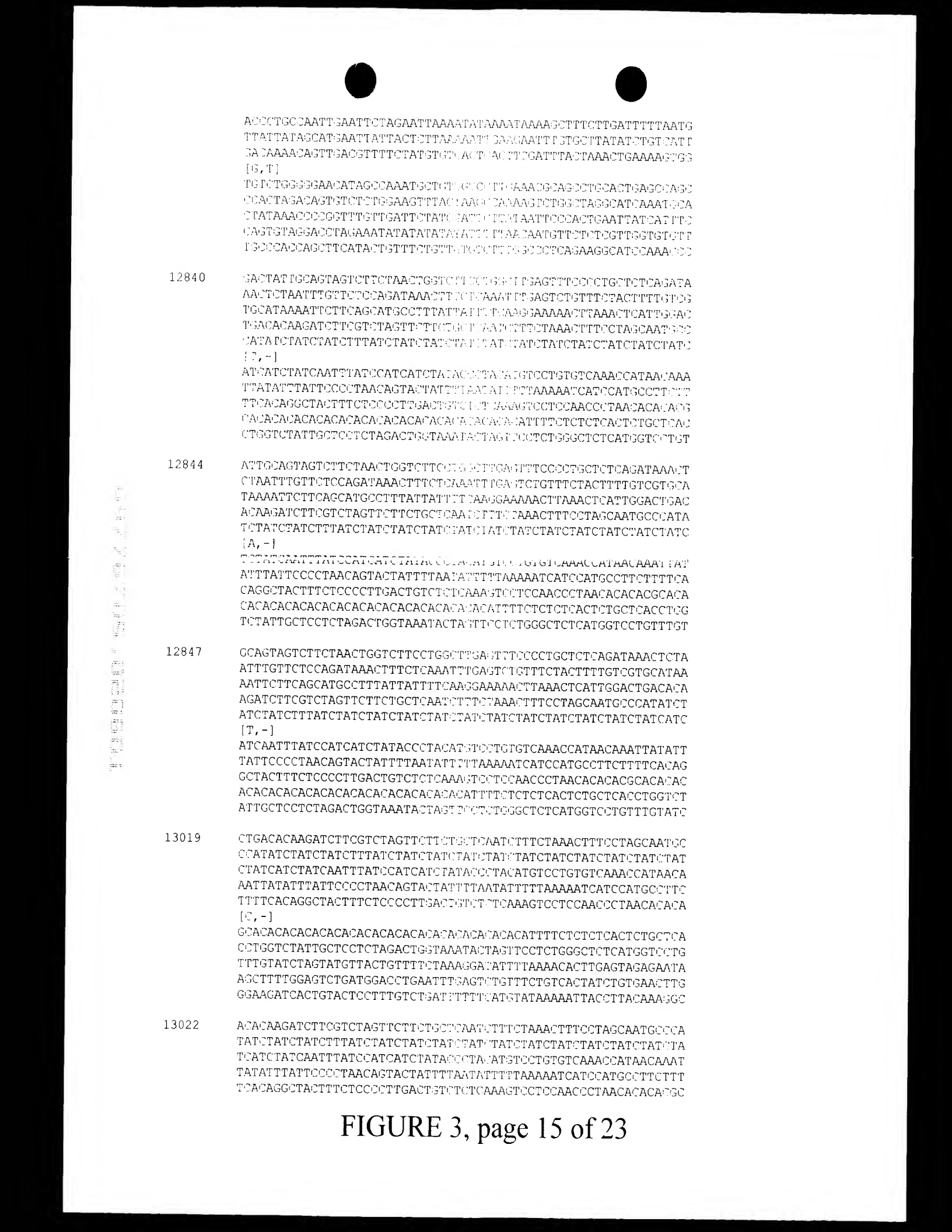

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[G,T]
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Replacement Sheet

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